Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 10:07:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068102.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6068102 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068102.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 10:07:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068102.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,123,846
Mapped reads	3,828,111 / 92.83%
Unmapped reads	295,735 / 7.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,479 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	382,420 / 9.27%
Duplication rate	8.44%
Clipped reads	2,115,445 / 51.3%

2.2. ACGT Content

Number/percentage of A's	64,131,338 / 26.28%
Number/percentage of C's	43,380,017 / 17.78%
Number/percentage of T's	79,500,648 / 32.58%
Number/percentage of G's	56,993,713 / 23.35%
Number/percentage of N's	27,834 / 0.01%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0789

Standard Deviation	0.7261

2.4. Mapping Quality

Mean Mapping Quality	44.33

2.5. Mismatches and indels

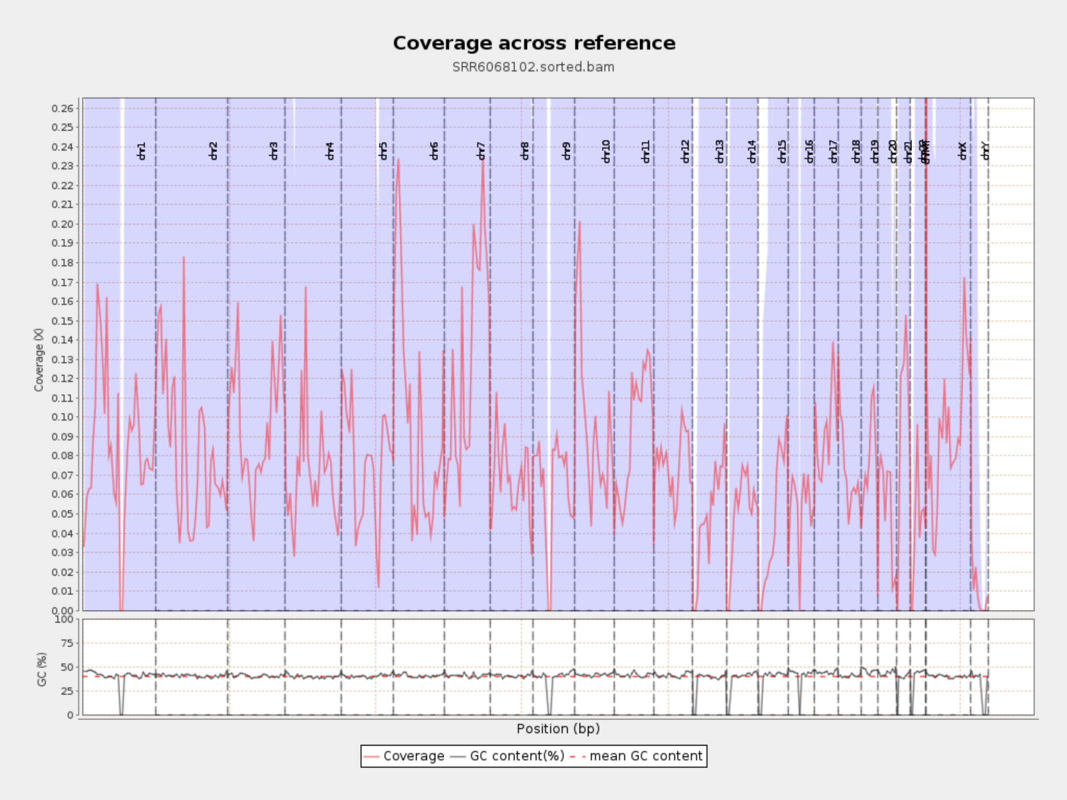
General error rate	0.56%
Mismatches	1,330,389
Insertions	15,142
Mapped reads with at least one insertion	0.39%
Deletions	55,312
Mapped reads with at least one deletion	1.43%
Homopolymer indels	45.14%

2.6. Chromosome stats

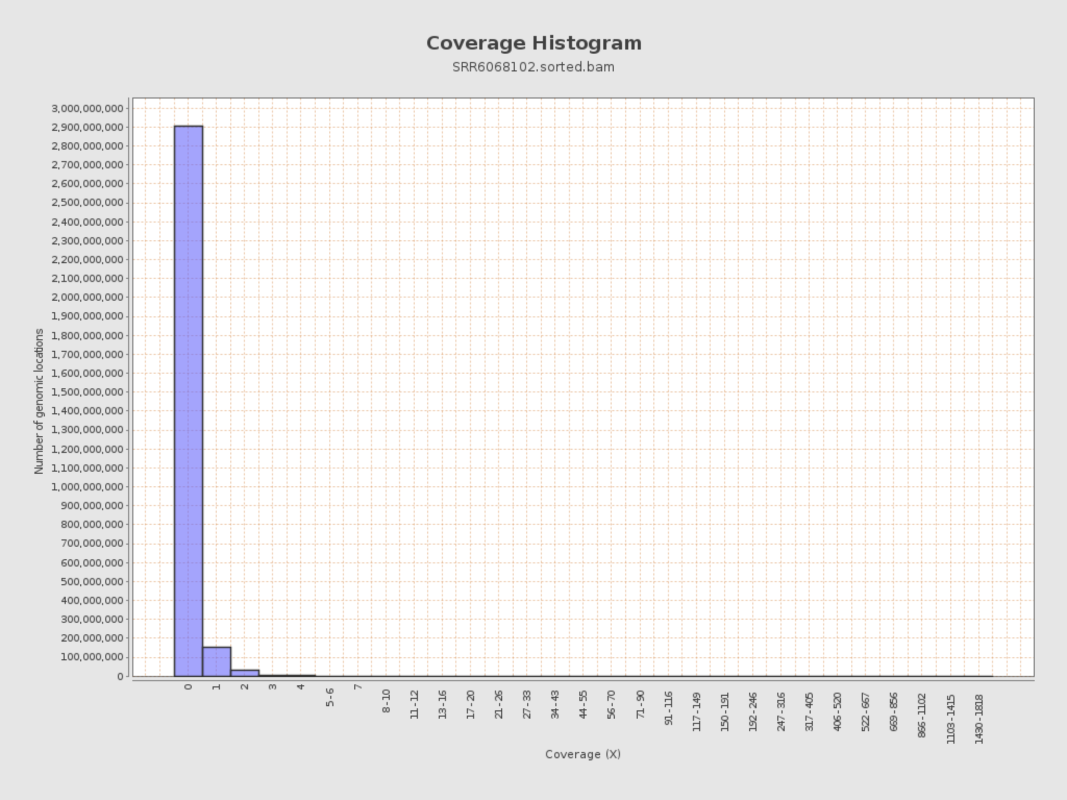
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	21004160	0.0843	1.2321
chr2	243199373	20388791	0.0838	1.103
chr3	198022430	18978181	0.0958	0.3825
chr4	191154276	13566196	0.071	0.3456
chr5	180915260	14024583	0.0775	0.352
chr6	171115067	16911461	0.0988	0.5168
chr7	159138663	20612547	0.1295	1.3932

chr8	146364022	9938413	0.0679	0.7752
chr9	141213431	9100826	0.0644	0.6867
chr10	135534747	13331625	0.0984	0.5083
chr11	135006516	12548873	0.093	0.6002
chr12	133851895	10225685	0.0764	0.3821
chr13	115169878	5693371	0.0494	0.3023
chr14	107349540	5432477	0.0506	0.3772
chr15	102531392	4590569	0.0448	0.3162
chr16	90354753	4728584	0.0523	0.336
chr17	81195210	7724271	0.0951	0.4332
chr18	78077248	5656843	0.0725	1.1501
chr19	59128983	4515532	0.0764	0.8768
chr20	63025520	3307185	0.0525	0.3226
chr21	48129895	4680128	0.0972	0.4093
chr22	51304566	2162851	0.0422	0.2473
chrMT	16571	132681	8.0068	5.1766
chrX	155270560	14315154	0.0922	0.4981
chrY	59373566	558047	0.0094	0.1786

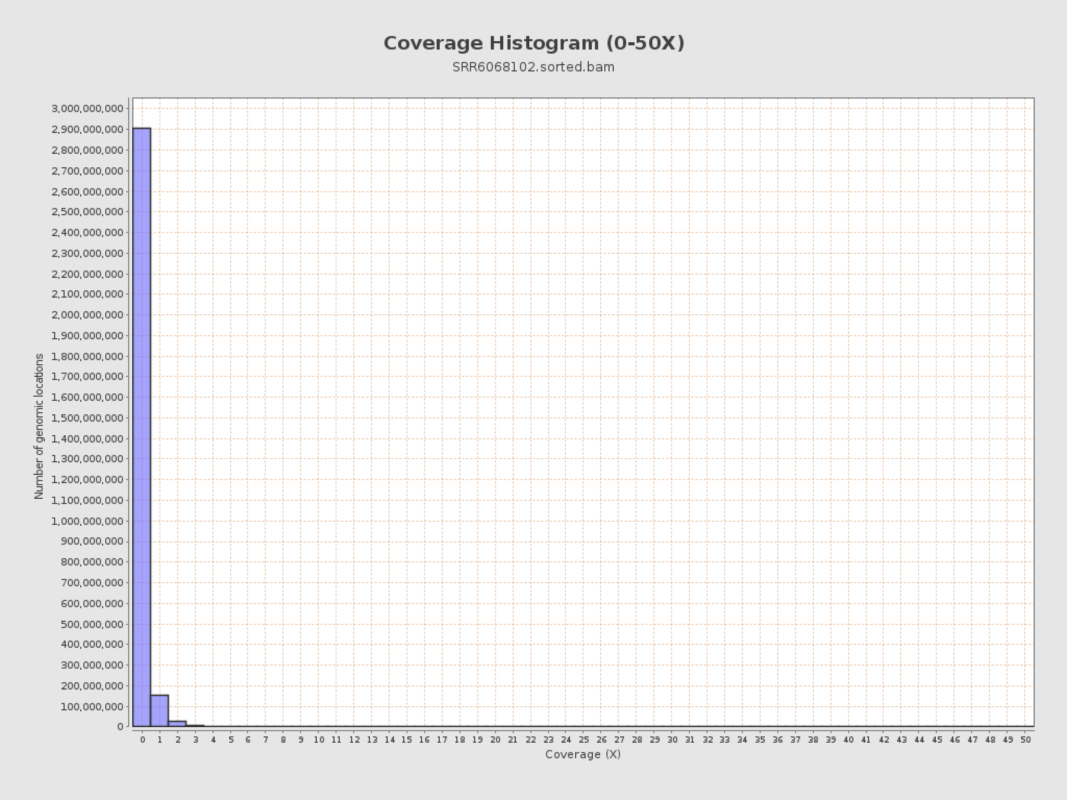
3. Results : Coverage across reference



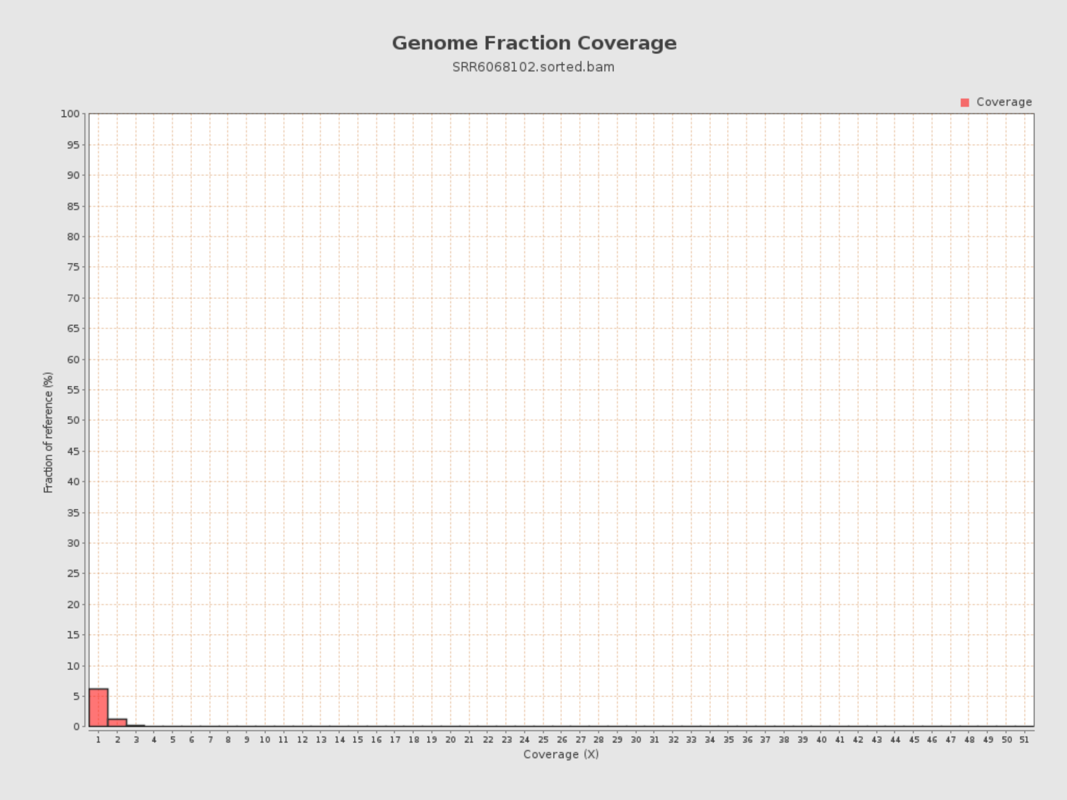
4. Results : Coverage Histogram



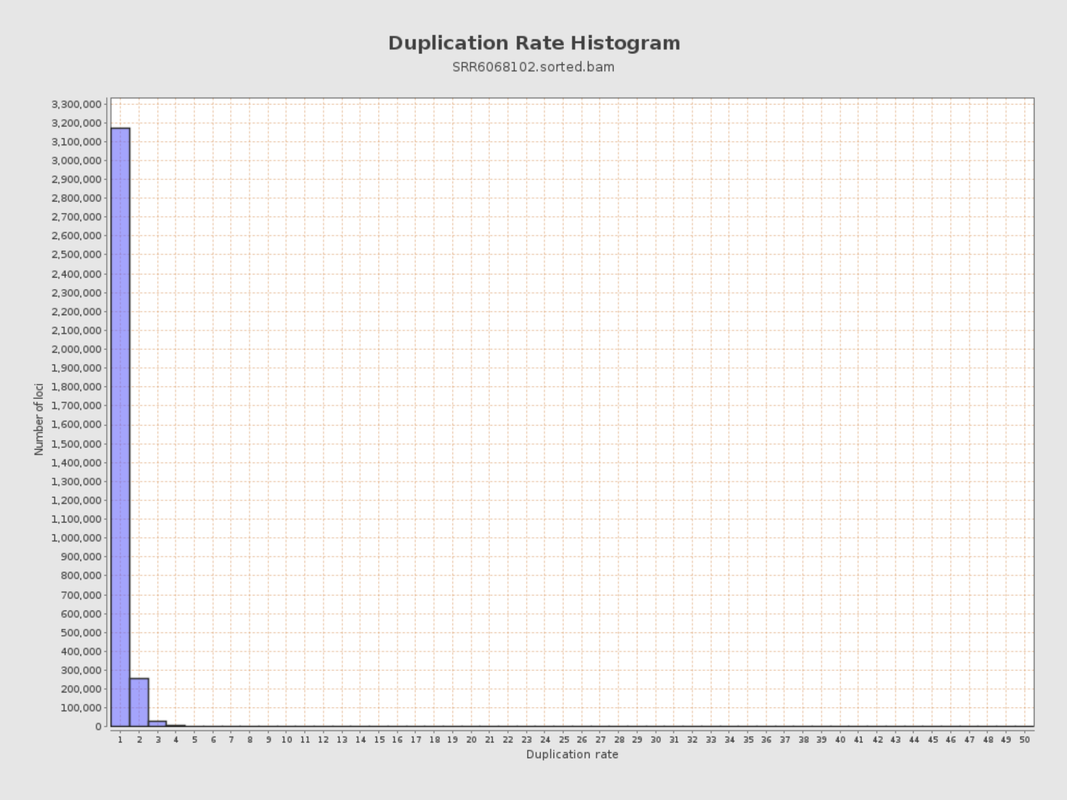
5. Results : Coverage Histogram (0-50X)



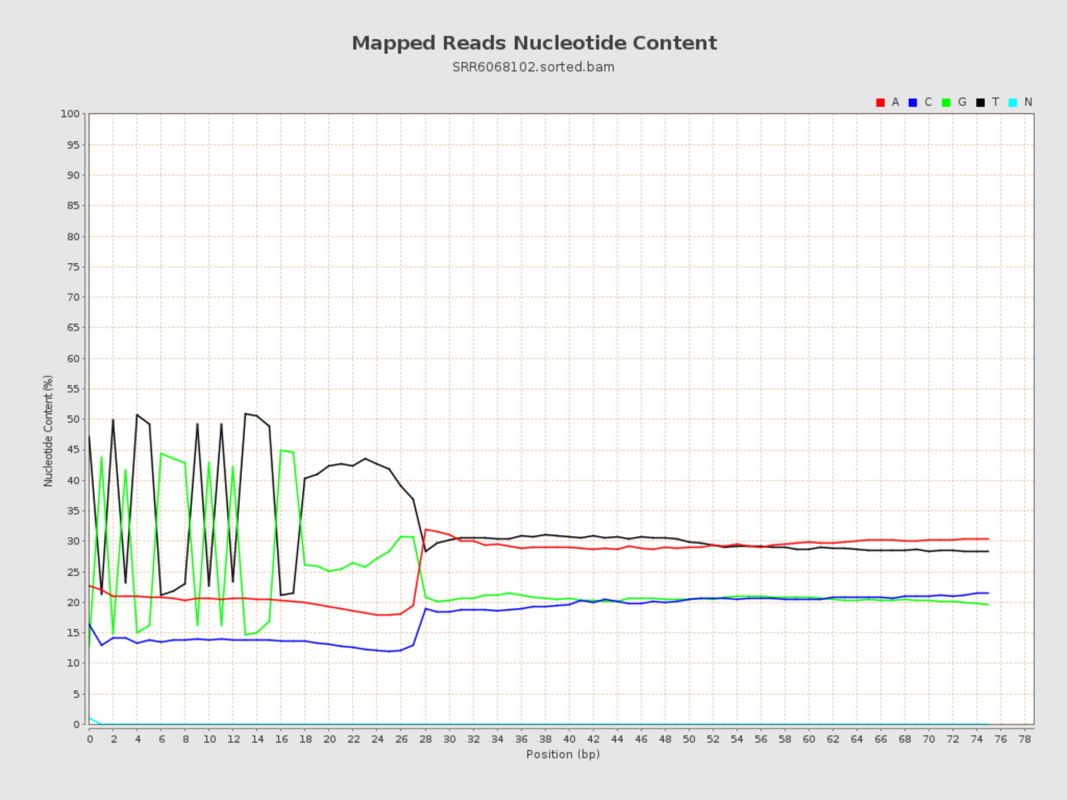
6. Results : Genome Fraction Coverage



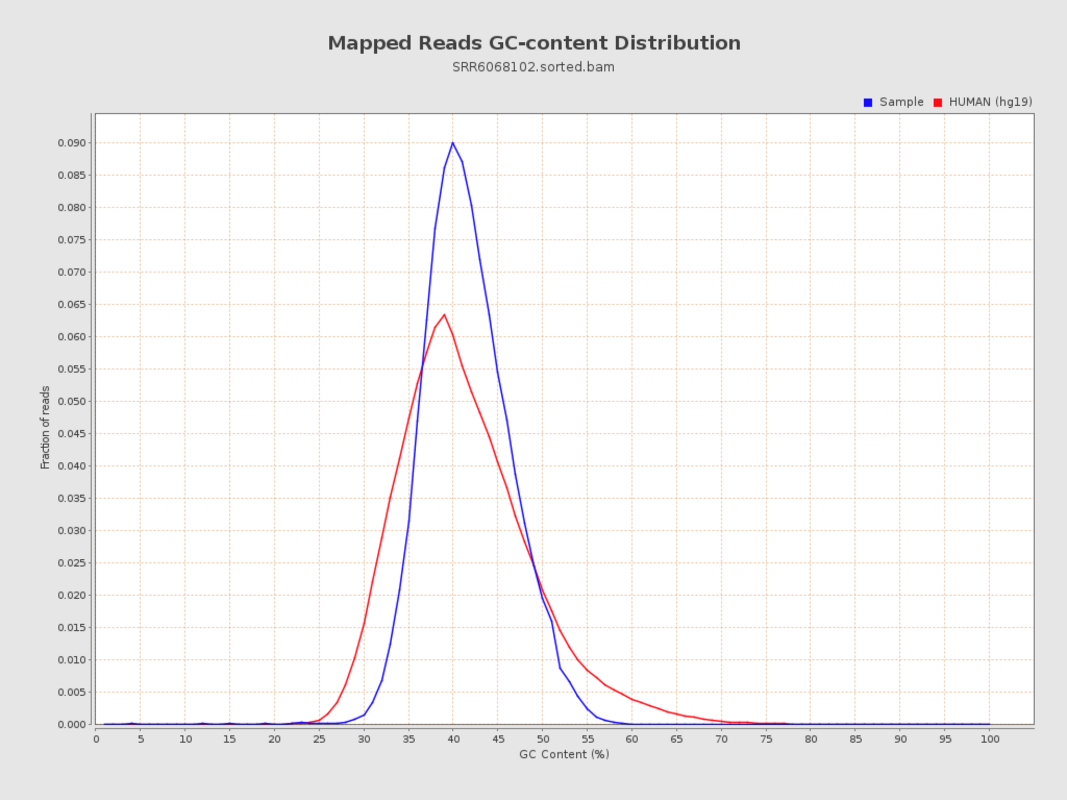
7. Results : Duplication Rate Histogram



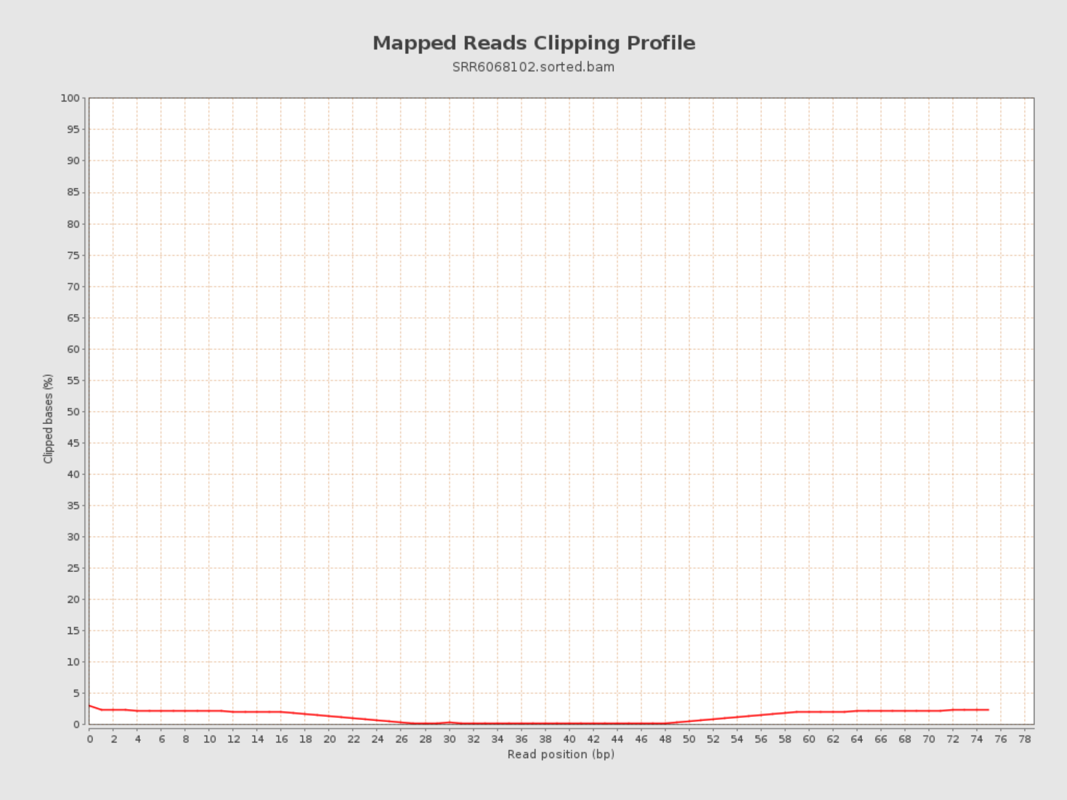
8. Results : Mapped Reads Nucleotide Content



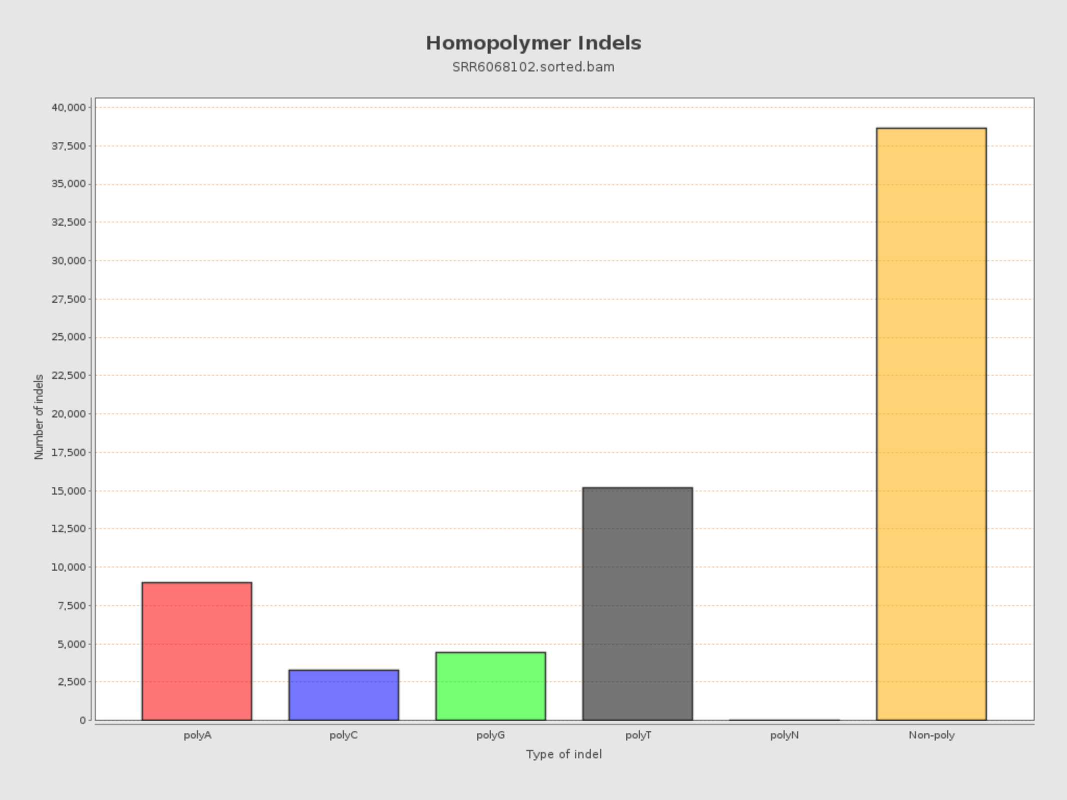
9. Results : Mapped Reads GC-content Distribution



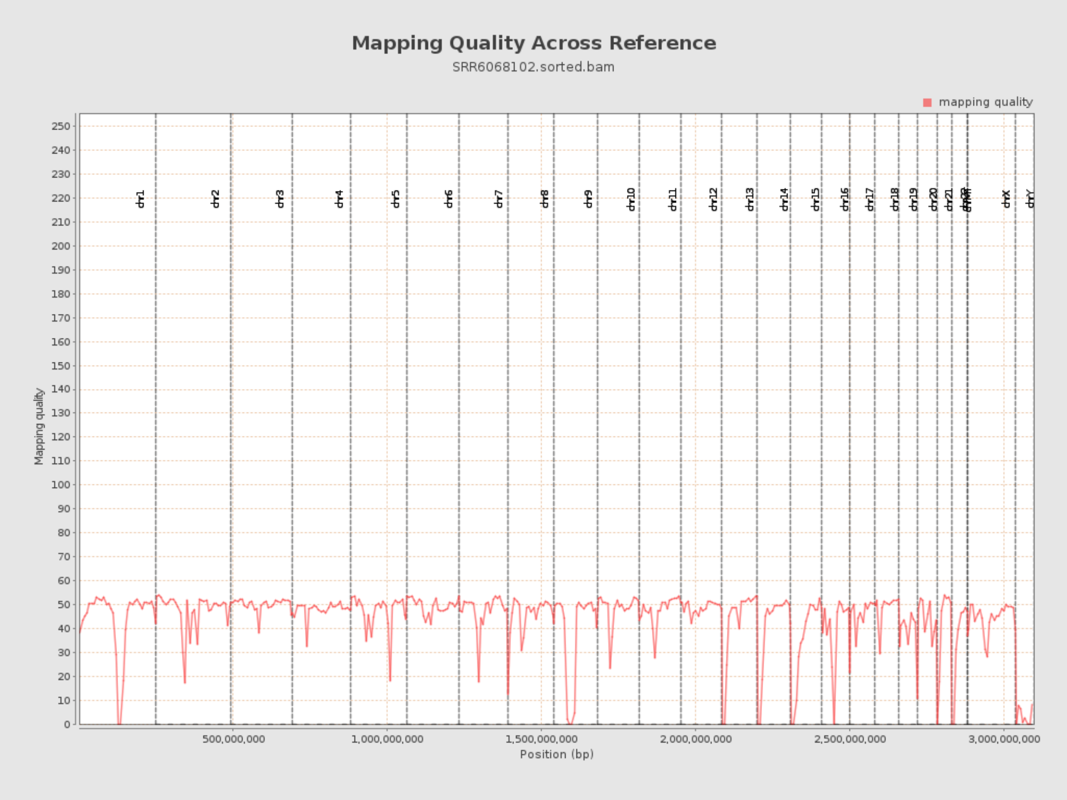
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram